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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=8; day=14; hr=19; min=28; sec=49; ms=16; ]

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Application No: 10594349 Version No: 2.0

**Input Set:****Output Set:**

**Started:** 2008-07-14 20:25:35.598  
**Finished:** 2008-07-14 20:25:39.452  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 854 ms  
**Total Warnings:** 7  
**Total Errors:** 12  
**No. of SeqIDs Defined:** 18  
**Actual SeqID Count:** 18

| Error code | Error Description  |
|------------|--|
| E 355      | Empty lines found between the amino acid numbering and the     |
| E 321      | No. of Bases conflict, this line has no nucleotides SEQID (4)  |
| E 355      | Empty lines found between the amino acid numbering and the     |
| E 321      | No. of Bases conflict, this line has no nucleotides SEQID (6)  |
| E 355      | Empty lines found between the amino acid numbering and the     |
| E 321      | No. of Bases conflict, this line has no nucleotides SEQID (6)  |
| E 355      | Empty lines found between the amino acid numbering and the     |
| E 321      | No. of Bases conflict, this line has no nucleotides SEQID (8)  |
| E 355      | Empty lines found between the amino acid numbering and the     |
| E 321      | No. of Bases conflict, this line has no nucleotides SEQID (11) |
| E 355      | Empty lines found between the amino acid numbering and the     |
| E 321      | No. of Bases conflict, this line has no nucleotides SEQID (11) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (12)            |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (13)            |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (14)            |
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| W 213      | Artificial or Unknown found in <213> in SEQ ID (17)            |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (18)            |



# SEQUENCE LISTING

<110> NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND  
TECHNOLOGY  
MIYAKE, Masato  
YOSHIKAWA, Tomohiro  
UCHIMURA, Eiichiro  
MIYAKE, Jun

<120> COMPOSITION AND METHOD FOR INCREASING EFFICIENCY  
OF INTRODUCTION OF TARGET SUBSTANCE INTO CELL

<130> 690121.410USPC

<140> 10594349

<141> 2008-07-14

<150> PCT/JP2004/002696

<151> 2004-03-03

<150> JP2003-057869

<151> 2003-03-04

<160> 18

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<212> DNA

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<221> CDS

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<223> fibronectin 1

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ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg cag 96

Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln

20 25 30

gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa agc 144

Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser

35 40 45

aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa cag 192

Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln

50 55 60

tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat gga 240

Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly

65 70 75 80

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|---|-----|
| gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag act | 288 |
| Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr |     |
| 85 90 95  |     |
| tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act tat | 336 |
| Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr |     |
| 100 105 110   |     |
| gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg gct | 384 |
| Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala |     |
| 115 120 125   |     |
| ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa ggg | 432 |
| Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly |     |
| 130 135 140   |     |
| ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag act | 480 |
| Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr |     |
| 145 150 155 160   |     |
| ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga gaa | 528 |
| Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu |     |
| 165 170 175   |     |
| tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct ggg | 576 |
| Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly |     |
| 180 185 190   |     |
| act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc tgg | 624 |
| Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp |     |
| 195 200 205   |     |
| atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc act | 672 |
| Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr |     |
| 210 215 220   |     |
| tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc tat | 720 |
| Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr |     |
| 225 230 235 240   |     |
| aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg ctc | 768 |
| Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu |     |
| 245 250 255   |     |
| cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag agg | 816 |
| Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg |     |
| 260 265 270   |     |
| cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc gat | 864 |
| His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp |     |
| 275 280 285   |     |
| gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct ccc | 912 |
| Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro |     |
| 290 295 300   |     |

|   |      |
|---|------|
| tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg atg | 960  |
| Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met |      |
| 305 310 315 320   |      |
| cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc ctg | 1008 |
| Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu |      |
| 325 330 335   |      |
| ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac ggt | 1056 |
| Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly |      |
| 340 345 350   |      |
| ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat ggc | 1104 |
| Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly |      |
| 355 360 365   |      |
| agg acg gac agc aca act tcg aat tat gag cag gac cag aaa tac tct | 1152 |
| Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser |      |
| 370 375 380   |      |
| ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc | 1200 |
| Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser |      |
| 385 390 395 400   |      |
| aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac | 1248 |
| Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr |      |
| 405 410 415   |      |
| act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg | 1296 |
| Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly |      |
| 420 425 430   |      |
| acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg | 1344 |
| Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met |      |
| 435 440 445   |      |
| gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc | 1392 |
| Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg |      |
| 450 455 460   |      |
| att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg | 1440 |
| Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg |      |
| 465 470 475 480   |      |
| tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac | 1488 |
| Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr |      |
| 485 490 495   |      |
| tcg cag ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg | 1536 |
| Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val |      |
| 500 505 510   |      |
| aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt | 1584 |
| Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys |      |
| 515 520 525   |      |
| aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac | 1632 |

|   |             |
|---|-------------|
| Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp |             |
| 530   | 540         |
|   |             |
| caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca | 1680        |
| Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser |             |
| 545   | 550 555 560 |
|   |             |
| tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc | 1728        |
| Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly |             |
| 565   | 570 575     |
|   |             |
| cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc | 1776        |
| Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser |             |
| 580   | 585 590     |
|   |             |
| tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc | 1824        |
| Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro |             |
| 595   | 600 605     |
|   |             |
| aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc | 1872        |
| Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser |             |
| 610   | 615 620     |
|   |             |
| aag tac att ctc agg tgg aga cct gtg agt atc cca ccc aga aac ctt | 1920        |
| Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu |             |
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| gga tac tga   | 1929        |
| Gly Tyr   |             |

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 <213> Homo sapiens

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| 20  | 25 30    |
|   |          |
| Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser |          |
| 35  | 40 45    |
|   |          |
| Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln |          |
| 50  | 55 60    |
|   |          |
| Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly |          |
| 65  | 70 75 80 |

Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
85 90 95

Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
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Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
115 120 125

Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
130 135 140

Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
145 150 155 160

Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
165 170 175

Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly  
180 185 190

Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp  
195 200 205

Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr  
210 215 220

Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr  
225 230 235 240

Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu  
245 250 255

Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg  
260 265 270

His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp  
275 280 285

Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro  
290 295 300



Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met  
305 310 315 320

Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu  
325 330 335

Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly  
340 345 350

Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly  
355 360 365

Arg Thr Asp Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser  
370 375 380

Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser  
385 390 395 400

Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr  
405 410 415

Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly  
420 425 430

Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met  
435 440 445

Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg  
450 455 460

Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg  
465 470 475 480

Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr  
485 490 495

Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val  
500 505 510

Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys  
515 520 525

Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp  
530 535 540

Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser  
545 550 555 560

Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly  
565 570 575

Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser  
580 585 590

Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro  
595 600 605

Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser  
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Gly Tyr

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tct ctg gct gac caa gag tca tgc aag ggc cgc tgc act cag ggt ttc 96  
Ser Leu Ala Asp Gln Glu Ser Cys Lys Gly Arg Cys Thr Gln Gly Phe  
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atg gcc agc aag aag tgt cag tgt gac gag ctt tgc act tac tat cag 144  
Met Ala Ser Lys Lys Cys Gln Cys Asp Glu Leu Cys Thr Tyr Tyr Gln  
35 40 45

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| agc tgc tgt gcc gac tac atg gag cag tgc aag ccc caa gta acg cgg | 192 |
| Ser Cys Cys Ala Asp Tyr Met Glu Gln Cys Lys Pro Gln Val Thr Arg |     |
| 50 55 60  |     |
| ggg gac gtg ttc act atg cca gag gat gat tat tgg agc tat gac tac | 240 |
| Gly Asp Val Phe Thr Met Pro Glu Asp Asp Tyr Trp Ser Tyr Asp Tyr |     |
| 65 70 75 80   |     |
| gtg gag gag ccc aag aac aat acc aac acc ggt gtg caa ccc gag aac | 288 |
| Val Glu Glu Pro Lys Asn Asn Thr Asn Thr Gly Val Gln Pro Glu Asn |     |
| 85 90 95  |     |
| acc tct cca ccc ggt gac cta aat cct cgg acg gac ggc act cta aag | 336 |
| Thr Ser Pro Pro Gly Asp Leu Asn Pro Arg Thr Asp Gly Thr Leu Lys |     |
| 100 105 110   |     |
| ccg aca gcc ttc cta gat cct gag gaa cag cca agc acc cca gcg cct | 384 |
| Pro Thr Ala Phe Leu Asp Pro Glu Glu Gln Pro Ser Thr Pro Ala Pro |     |
| 115 120 125   |     |
| aaa gtg gag caa cag gag gag atc cta agg ccc gac acc act gat caa | 432 |
| Lys Val Glu Gln Gln Glu Glu Ile Leu Arg Pro Asp Thr Thr Asp Gln |     |
| 130 135 140   |     |
| ggg acc cct gag ttt cca gag gaa gaa ctg tgc agt gga aag ccc ttt | 480 |
| Gly Thr Pro Glu Phe Pro Glu Glu Glu Leu Cys Ser Gly Lys Pro Phe |     |
| 145 150 155 160   |     |
| gac gcc ttc acg gat ctc aag aat ggg tcc ctc ttt gcc ttc cga ggg | 528 |
| Asp Ala Phe Thr Asp Leu Lys Asn Gly Ser Leu Phe Ala Phe Arg Gly |     |
| 165   |     |